

## WEST Search History





DATE: Monday, January 23, 2006

<b>Hide?</b>	<b>Set Name</b>	<b>Query</b>	<b>Hit Count</b>
	<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L34	L27 and probe	1
<input type="checkbox"/>	L33	L27 and complementary	0
<input type="checkbox"/>	L32	6316272.pn.	1
<input type="checkbox"/>	L31	L30 not @ay>2001	20
<input type="checkbox"/>	L30	L1 and (prostate or colon)	39
<input type="checkbox"/>	L29	L28 not @ay>2001	20
<input type="checkbox"/>	L28	L3 and (prostate or colon)	39
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<input type="checkbox"/>	L24	colorectal.ti.	208
<input type="checkbox"/>	L23	L22 and (prostate or colon)	0
<input type="checkbox"/>	L22	6235879.pn.	1
<input type="checkbox"/>	L21	L20 and L14	2
<input type="checkbox"/>	L20	L19 and L12	4
<input type="checkbox"/>	L19	(ross or mizukami or Rao).in.	21320
<input type="checkbox"/>	L18	L2 and L12	6
<input type="checkbox"/>	L17	L13 and (prostate or colon)	3
<input type="checkbox"/>	L16	L15 and (prostate or colon)	2
<input type="checkbox"/>	L15	L13 and L14	2
<input type="checkbox"/>	L14	L2.clm.	37914
<input type="checkbox"/>	L13	L3 and L12	6
<input type="checkbox"/>	L12	L7 or L8 or L10	8
<input type="checkbox"/>	L11	L7 or L8 or L10L10	5
<input type="checkbox"/>	L10	L1.ab.	7
<input type="checkbox"/>	L9	L1.ab. L8	8
<input type="checkbox"/>	L8	L1.ti.	4
<input type="checkbox"/>	L7	L1.clm.	3
<input type="checkbox"/>	L6	L5 and (screen\$ or detect\$ or determin\$ or diagnos\$)	34
<input type="checkbox"/>	L5	L3 and L4	34
<input type="checkbox"/>	L4	@AY <= 2001	5488050

<input type="checkbox"/>	L3	L1 and L2	70
<input type="checkbox"/>	L2	cancer\$ or neoplas\$ or angiogen\$ or tumor\$	184538
<input type="checkbox"/>	L1	hip1 or (huntington adj interacting adj protein)	81

END OF SEARCH HISTORY

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 11:00:20 ; Search time 14682 Seconds  
 (without alignments)  
 17554.026 Million cell updates/sec

Title: US-10-007-047-1  
 Perfect score: 4534  
 Sequence: 1 ccaagcttggtacccccggg.....gcatgcnntagagggcccta 4534

Scoring table: OLIGO\_NUC  
 Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*  
 1: gb\_ba:\*  
 2: gb\_in:\*  
 3: gb\_env:\*  
 4: gb\_om:\*  
 5: gb\_ov:\*  
 6: gb\_pat:\*  
 7: gb\_ph:\*  
 8: gb\_pr:\*  
 9: gb\_ro:\*  
 10: gb\_sts:\*  
 11: gb\_sy:\*  
 12: gb\_un:\*  
 13: gb\_vi:\*  
 14: gb\_htg:\*  
 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3035	66.9	4714	8	HSU79734	U79734 Human hunti
2	3035	66.9	6626	6	AX828392	AX828392 Sequence

	3	3028	66.8	4707	6	CQ728008	CQ728008	Sequence
	4	2940	64.8	3093	8	AF365404	AF365404	Homo sapi
	5	2619	57.8	4796	6	AR153626	AR153626	Sequence
	6	2619	57.8	4796	6	BD227037	BD227037	Apoptosis
	7	1162	25.6	1201	8	HSHIPIPRO	Y09420	H.sapiens m
	8	973	21.5	134979	8	AC018720	AC018720	Homo sapi
	9	955	21.1	3715	6	AR153661	AR153661	Sequence
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	11	955	21.1	3715	8	HSAHIPI28	AF052288	Homo sapi
c	12	922	20.3	180399	14	AC079252	AC079252	Homo sapi
	13	907	20.0	1164	6	AR153625	AR153625	Sequence
	14	907	20.0	1164	6	BD227036	BD227036	Apoptosis
c	15	740	16.3	183915	14	AC073967	AC073967	Homo sapi
	16	554	12.2	601	6	AX321326	AX321326	Sequence
c	17	394	8.7	5853	6	AX828539	AX828539	Sequence
c	18	393	8.7	393	6	AX828493	AX828493	Sequence
	19	331	7.3	331	6	AX321316	AX321316	Sequence
	20	322	7.1	2440	8	AB179164	AB179164	Macaca fa
c	21	310	6.8	172105	8	AC093135	AC093135	Pan trogl
c	22	310	6.8	199670	8	AC142303	AC142303	Pan trogl
c	23	310	6.8	221091	8	AC146228	AC146228	Pan trogl
	24	259	5.7	518	6	CQ102544	CQ102544	Sequence
	25	259	5.7	518	6	CQ141451	CQ141451	Sequence
	26	259	5.7	518	6	CQ224738	CQ224738	Sequence
	27	259	5.7	518	6	CQ299810	CQ299810	Sequence
	28	259	5.7	518	6	CQ336990	CQ336990	Sequence
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	36	184	4.1	184	6	CQ312242	CQ312242	Sequence
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	44	161	3.6	161	8	AF486833	AF486833	Homo sapi
c	45	161	3.6	243	10	G30915	G30915	sWSS3387 Er

#### ALIGNMENTS

#### RESULT 1

HSU79734

LOCUS HSU79734 4714 bp mRNA linear PRI 06-MAY-1997  
DEFINITION Human huntingtin interacting protein (HIP1) mRNA, complete cds.  
ACCESSION U79734  
VERSION U79734.1 GI:2072422  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 4714)

AUTHORS Kalchman,M.A., Koide,H.B., McCutcheon,K., Graham,R.K., Nichol,K.,  
Nishiyama,K., Kazemi-Esfarjani,P., Lynn,F.C., Wellington,C.,  
Metzler,M., Goldberg,Y.P., Kanazawa,I., Geitz,R.D. and Hayden,M.R.  
TITLE HIP1, a human homologue of *S. cerevisiae* Sla2p, interacts with  
membrane-associated huntingtin in the brain

JOURNAL Nat. Genet. 16 (1), 44-53 (1997)

PUBMED 9140394

REFERENCE 2 (bases 1 to 4714)

AUTHORS Kalchman,M.A., Nichol,K., Graham,R.K., Geitz,R.D. and Hayden,M.R.

TITLE Direct Submission

JOURNAL Submitted (24-NOV-1996) Medical Genetics, University of British  
Columbia, #416-2125 East Mall, NCE Building, Vancouver, BC V6T 1Z4,  
Canada

FEATURES Location/Qualifiers

source

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/map="7q11.2"

gene

1. .4714  
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CDS

245. .2989  
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and ZK370.3 protein in *Caenorhabditis elegans*, encoded by  
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ORIGIN

Query Match 66.9%; Score 3035; DB 8; Length 4714;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 3135; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	183	CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACAGCCAGAAC	242
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Qy	243	GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG	302
Db	61	GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG	120
Qy	303	CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAACT	362
Db	121	CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAACT	180
Qy	363	CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG	422
Db	181	CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG	240
Qy	423	TGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA	482
Db	241	TGACATGAGCAGGATGTGGGGCCACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA	300
Qy	483	CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA	542
Db	301	CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA	360
Qy	543	CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTC	602
Db	361	CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTT	420
Qy	603	CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACCTCAACCTCTTCCAAACAGT	662
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Qy	663	ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT	722
Db	481	ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT	540
Qy	723	CGCCCCGCTGATCCAGGTCATCTTGACTGCAGCCACCTTTATGACTACACTGTCAAGCT	782
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Qy	783	TCTCTTCAAACCTCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT	842
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Qy	843	CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT	902
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Qy	903	CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACCTCCTGCGAGCCTC	962
Db	721	CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACCTCCTGCGAGCCTC	780
Qy	963	AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCGA	1022
Db	781	AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCGA	840

Qy	1023	CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT	1082
Db	841	CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT	900
Qy	1083	ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT	1142
Db	901	ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT	960
Qy	1143	CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG	1202
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Db	1021	AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT	1080
Qy	1263	GCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT	1322
Db	1081	GCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT	1140
Qy	1323	GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG	1382
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Qy	1383	GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA	1442
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Qy	1503	CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC	1562
Db	1321	CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC	1380
Qy	1563	CCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA	1622
Db	1381	CCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA	1440
Qy	1623	CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT	1682
Db	1441	CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT	1500
Qy	1683	TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAACTTCTGCCCAGTC	1742
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Qy	1803	TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAGAAGTGCAGGACACTCA	1862
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Qy	1863	GCTCAAAC TGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT	1922
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Qy	1923	GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT	1982
Db	1741	GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT	1800
Qy	1983	TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC	2042
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Qy	2163	CATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGAC	2222
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Qy	2223	CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA	2282
Db	2041	CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA	2100
Qy	2283	GGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGC	2342
Db	2101	GGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGC	2160
Qy	2343	CATCGGCAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCT	2402
Db	2161	CATCGGCAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCT	2220
Qy	2403	GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA	2462
Db	2221	GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA	2280
Qy	2463	GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG	2522
Db	2281	GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG	2340
Qy	2523	GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA	2582
Db	2341	GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA	2400
Qy	2583	GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTA	2642
Db	2401	GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTA	2460
Qy	2643	TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG	2702
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Qy	2703	AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA	2762



Db	2521	AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA	2580
Qy	2763	GCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA	2822
Db	2581	GCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA	2640
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Qy	2883	GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCGGCAAATCACAGATCGAAGA	2942
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Db	3001	CACCCCATATGTCAGTGTAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA	3060
Qy	3243	CAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGG	3302
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Qy	3303	ACATGCATGACACTTCC	3319
Db	3121	ACATGCATGACACTTCC	3137

## RESULT 2

AX828392

LOCUS AX828392 6626 bp DNA linear PAT 12-DEC-2003

DEFINITION Sequence 38 from Patent WO03074073.

ACCESSION AX828392

VERSION AX828392.1 GI:39838392

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1

AUTHORS Al-Mahmood,S., Colin,S. and Schneider,C.  
 TITLE Genes involved in regulating angiogenesis, pharmaceutical preparations containing same and applications thereof  
 JOURNAL Patent: WO 03074073-A 38 12-SEP-2003;  
 Gene Signal (FR)

FEATURES Location/Qualifiers  
 source 1. .6626  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 66.9%; Score 3035; DB 6; Length 6626;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3135; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	183	CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC	242
Db	1	CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC	60
Qy	243	GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG	302
Db	61	GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG	120
Qy	303	CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCACAAACT	362
Db	121	CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCACAAACT	180
Qy	363	CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG	422
Db	181	CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG	240
Qy	423	TGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA	482
Db	241	TGACATGAGCAGGATGTGGGGCCACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA	300
Qy	483	CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA	542
Db	301	CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA	360
Qy	543	CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTC	602
Db	361	CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTT	420
Qy	603	CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT	662
Db	421	CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT	480
Qy	663	ATTCAACTCCCTGGACATGTCCCCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT	722
Db	481	ATTCAACTCCCTGGACATGTCCCCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT	540
Qy	723	CGCCCCGCTGATCCAGGTCATCTTGACTGCAGCCACCTTTATGACTACACTGTCAAGCT	782
Db	541	CGCCCCGCTGATCCAGGTCATCTTGACTGCAGCCACCTTTATGACTACACTGTCAAGCT	600
Qy	783	TCTCTTCAAACCTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT	842

Db	601	 TCTCTTCAAACCTCCACTCCTGCCTCCCAGCTGACACCTGCAAGGCCACCGGGACCGCTT	660
Qy	843	CATGGAGCAGTTTACAAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT	902
Db	661	 CATGGAGCAGTTTACAAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT	720
Qy	903	CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACCTCCTGCGAGCCTC	962
Db	721	 CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACCTCCTGCGAGCCTC	780
Qy	963	AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCCTCATCCCCGA	1022
Db	781	 AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCCTCATCCCCGA	840
Qy	1023	CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT	1082
Db	841	 CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT	900
Qy	1083	ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTGAGCAGTGATCCCTTCAATTT	1142
Db	901	 ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTGAGCAGTGATCCCTTCAATTT	960
Qy	1143	CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG	1202
Db	961	 CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG	1020
Qy	1203	AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT	1262
Db	1021	 AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT	1080
Qy	1263	GCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT	1322
Db	1081	 GCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT	1140
Qy	1323	GCGGCAGCAGGCGGCCGACGACTGTGAATTCTGCGGGCAGAACTGGACGAGCTCAGGAG	1382
Db	1141	 GCGGCAGCAGGCGGCCGACGACTGTGAATTCTGCGGGCAGAACTGGACGAGCTCAGGAG	1200
Qy	1383	GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA	1442
Db	1201	 GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA	1260
Qy	1443	AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA	1502
Db	1261	 AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA	1320
Qy	1503	CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC	1562
Db	1321	 CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC	1380
Qy	1563	CCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA	1622
Db	1381	 CCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA	1440
Qy	1623	CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT	1682

Db	1441	CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT	1500
Qy	1683	TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC	1742
Db	1501	TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC	1560
Qy	1743	AGAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG	1802
Db	1561	AGAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG	1620
Qy	1803	TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA	1862
Db	1621	TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA	1680
Qy	1863	GCTCAAACCTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT	1922
Db	1681	GCTCAAACCTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT	1740
Qy	1923	GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT	1982
Db	1741	GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT	1800
Qy	1983	TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC	2042
Db	1801	TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC	1860
Qy	2043	ATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCC	2102
Db	1861	ATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCC	1920
Qy	2103	AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC	2162
Db	1921	AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC	1980
Qy	2163	CATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGAC	2222
Db	1981	CATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGAC	2040
Qy	2223	CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA	2282
Db	2041	CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA	2100
Qy	2283	GGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGC	2342
Db	2101	GGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGC	2160
Qy	2343	CATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCT	2402
Db	2161	CATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCT	2220
Qy	2403	GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA	2462
Db	2221	GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA	2280
Qy	2463	GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG	2522
Db	2281	GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG	2340

Qy	2523	GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA	2582
Db	2341	GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA	2400
Qy	2583	GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCCTAAAGAGTTTAA	2642
Db	2401	GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCCTAAAGAGTTTAA	2460
Qy	2643	TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG	2702
Db	2461	TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG	2520
Qy	2703	AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA	2762
Db	2521	AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA	2580
Qy	2763	GCTAATGGTGTGTTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA	2822
Db	2581	GCTAATGGTGTGTTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA	2640
Qy	2823	GGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGT	2882
Db	2641	GGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGT	2700
Qy	2883	GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGA	2942
Db	2701	GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGA	2760
Qy	2943	GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA	3002
Db	2761	GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA	2820
Qy	3003	TTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAAGTGGG	3062
Db	2821	TTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAAGTGGG	2880
Qy	3063	AGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAGGAAC	3122
Db	2881	AGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAGGAAC	2940
Qy	3123	AGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAA	3182
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Qy	3183	CACCCCATATGTCAGTGTAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA	3242
Db	3001	CACCCCATATGTCAGTGTAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA	3060
Qy	3243	CAGGCCAAATCCTTGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGG	3302
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Qy	3303	ACATGCATGACACTTCC	3319
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## CO728008

DEFINITION Sequence 13942 from Patent WO02068579.

VERSION CO728008.1 GI:42295624

## KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
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JOURNAL Patent: WO 02068579-A 13942 06-SEP-2002;  
PE Corporation (NY) (US)

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FEATURES                                Location/Qualifiers
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                                     /mol_type="unassigned DNA"
                                     /db_xref="taxon:9606"
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## ORIGIN

Query Match 66.8%; Score 3028; DB 6; Length 4707;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3178; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC 60

Qy 243 GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG 302

Db 61 GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG 120

QY 303 CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT 362

Db 121 CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT 180

Qy 363 CCTCCGAGATGGACACCCGAACGTCTCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG 422

Db 181 CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG 240

Qy 423 TGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA 482

Db 241 TGACATGAGCAGGATGTGGGGCCACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA 300

Qy 483 CCTGAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA 542

Db 301 CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA 360

Qy 543 CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACCTTTTC 602

Db	361	CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTT	420
Qy	603	CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT	662
Db	421	CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT	480
Qy	663	ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT	722
Db	481	ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT	540
Qy	723	CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT	782
Db	541	CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT	600
Qy	783	TCTCTTCAAACCTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT	842
Db	601	TCTCTTCAAACCTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT	660
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Qy	1023	CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT	1082
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Qy	1083	ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTGAGCAGTGATCCCTTCAATTT	1142
Db	901	ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTGAGCAGTGATCCCTTCAATTT	960
Qy	1143	CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG	1202
Db	961	CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG	1020
Qy	1203	AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT	1262
Db	1021	AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT	1080
Qy	1263	GCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT	1322
Db	1081	GCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT	1140
Qy	1323	GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG	1382
Db	1141	GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG	1200
Qy	1383	GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA	1442
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Qy	1443	AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA	1502
Db	1261	AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA	1320
Qy	1503	CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC	1562
Db	1321	CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC	1380
Qy	1563	CCAGGTAGATTTGGAACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA	1622
Db	1381	CCAGGTAGATTTGGAACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA	1440
Qy	1623	CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT	1682
Db	1441	CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT	1500
Qy	1683	TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC	1742
Db	1501	TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC	1560
Qy	1743	AGAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG	1802
Db	1561	AGAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG	1620
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Qy	1923	GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT	1982
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Qy	1983	TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC	2042
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Db	1861	ATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCC	1920
Qy	2103	AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC	2162
Db	1921	AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC	1980
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Db	1981	CATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGAC	2040
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Qy	2403	GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA	2462
Db	2221	GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA	2280
Qy	2463	GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG	2522
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Qy	2763	GCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA	2822
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Qy	2943	GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA	3002
Db	2761	GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA	2820
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Qy	3063	AGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAGGAAC	3122
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      |
Db      3181 G 3181

```

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 07:57:30 ; Search time 1667 Seconds  
(without alignments)  
18127.004 Million cell updates/sec

Title: US-10-007-047-1  
Perfect score: 4534  
Sequence: 1 ccaagcttggtacccccggg.....gcatgcnntagagggcccta 4534

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_21:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*

10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	% Query					Description
	No.	Score	Match	Length	ID	
	1	4534	100.0	4534	10	ACC85533 Human HIP
	2	4534	100.0	4534	14	Aeb71165 DNA encod
	3	3911	86.3	3911	10	ACC85534 Human HIP
	4	3911	86.3	3911	14	Aeb71167 DNA encod
	5	3079	67.9	6623	13	ACN38651 Tumour-as
	6	3079	67.9	6624	13	Adq86162 Human tum
	7	3035	66.9	6626	12	Adk60463 Angiogene
	8	3035	66.9	6626	12	Adk60764 Angiogene
	9	3035	66.9	6626	12	Adn01766 Human hun
	10	3035	66.9	6626	12	Adp73086 Angiogene
	11	3035	66.9	6626	13	Adp23862 PRO polyp
	12	2675	59.0	2745	14	Adv42966 Human psy
	13	2619	57.8	4796	2	Aat67187 Huntingti
	14	2619	57.8	4796	3	Aaz58746 Human hun
	15	1160	25.6	1173	14	Adv77138 Huntingto
	16	973	21.5	65454	12	Adn01773 Human hun
	17	955	21.1	3715	3	Aaz58781 Human HIP
	18	907	20.0	1164	2	Aat67186 Huntingti
	19	907	20.0	1164	3	Aaz58745 Human hun
	20	554	12.2	601	6	Aas61792 Lung smal
c	21	394	8.7	5853	12	Adk60309 Angiogene
c	22	394	8.7	5853	12	Adk60610 Angiogene
c	23	394	8.7	5853	12	Adp73233 Angiogene
c	24	393	8.7	393	12	Adk60263 Antisense
c	25	393	8.7	393	12	Adk60564 Antisense
c	26	393	8.7	393	12	Adp73187 Angiogene
c	27	363	8.0	482	10	Add32881 Human mit
	28	331	7.3	331	6	Aas61782 Lung smal
	29	259	5.7	518	4	Aai42717 Probe #11
	30	259	5.7	518	4	Aak36916 Human bon
	31	259	5.7	518	4	Aak11093 Human bra
	32	259	5.7	518	4	Abs36587 Human liv
	33	259	5.7	518	6	Abs10924 Human gen
	34	187	4.1	436	3	Aaz58765 Human hun
	35	184	4.1	184	4	Aai55778 Probe #24
	36	184	4.1	184	4	Aak49859 Human bon
	37	184	4.1	184	4	Aak23763 Human bra
	38	184	4.1	184	4	Abs49496 Human liv
	39	184	4.1	184	6	Abs23356 Human gen
	40	175	3.9	279	3	Aaz58780 Human hun
	41	163	3.6	404	10	Acc85536 Human HIP
	42	163	3.6	404	14	Aeb71169 DNA of HI

43	148	3.3	485	3	AAZ58769	Aaz58769 Human hun
44	144	3.2	565	3	AAZ58760	Aaz58760 Human hun
45	143	3.2	577	4	AAI17388	Aai17388 Probe #73

# ALIGNMENTS

## RESULT 1

ACC85533

ID ACC85533 standard; DNA; 4534 BP.

XX

AC ACC85533;

XX

DT 15-OCT-2003 (first entry)

XX

DE Human HIP1 cancer marker coding sequence.

XX

KW Human; HIP1; cancer; cancer marker; epithelial cancer; cytostatic; gene;  
KW ds.

XX

OS Homo sapiens.

XX

PN WO2003043566-A2.

XX

PD 30-MAY-2003.

XX

PF 12-NOV-2002; 2002WO-US036175.

XX

PR 15-NOV-2001; 2001US-0335276P.

PR 06-DEC-2001; 2001US-00007047.

XX

PA (UNMI ) UNIV MICHIGAN.

XX

PI Ross T, Mizukami I, Roa D;

XX

DR WPI; 2003-457565/43.

XX

PT New antibody binding to HIP1 but not to normal epithelium, useful for  
PT diagnosing and treating epithelial cancers, particularly colon and  
PT prostate cancer.

XX

PS Disclosure; Fig 7; 143pp; English.

XX

CC The present invention relates to an antibody that specifically binds to  
CC HIP1 but does not specifically bind to the normal epithelium of prostate  
CC or colon. The antibody can be used for diagnosing and treating epithelial  
CC cancers, particularly colon and prostate cancer. The present sequence is  
CC the human HIP1 coding sequence

XX

SQ Sequence 4534 BP; 1176 A; 1230 C; 1232 G; 894 T; 0 U; 2 Other;

Query Match 100.0%; Score 4534; DB 10; Length 4534;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCCTGACTCGGCTCCTCGGGCGACATG 60

Db	1		CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCTGACTCGGCTCCTCGCGGCACATG	60
Qy	61		GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG	120
Db	61		GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG	120
Qy	121		CGCGGGGTCGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT	180
Db	121		CGCGGGGTCGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT	180
Qy	181		GTCAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGA	240
Db	181		GTCAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGA	240
Qy	241		ACGTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAAC	300
Db	241		ACGTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAAC	300
Qy	301		CGCCTGCCCTCTGTCTAGCAACGCAGTGTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA	360
Db	301		CGCCTGCCCTCTGTCTAGCAACGCAGTGTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA	360
Qy	361		CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG	420
Db	361		CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG	420
Qy	421		AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC	480
Db	421		AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC	480
Qy	481		TACCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGC	540
Db	481		TACCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGC	540
Qy	541		AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACCTTT	600
Db	541		AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACCTTT	600
Qy	601		TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACCTCAACCTCTTCCAAACA	660
Db	601		TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACCTCAACCTCTTCCAAACA	660
Qy	661		GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC	720
Db	661		GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC	720
Qy	721		CTCGCCCCGCTGATCCAGGTCATCTTGACTGCAGCCACCTTTATGACTACACTGTCAAG	780
Db	721		CTCGCCCCGCTGATCCAGGTCATCTTGACTGCAGCCACCTTTATGACTACACTGTCAAG	780
Qy	781		CTTCTCTTCAAACCTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGC	840
Db	781		CTTCTCTTCAAACCTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGC	840
Qy	841		TTCATGGAGCAGTTTACAAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC	900

Db	841	TTCATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC	900
Qy	901	TTCAAGCGGCTCATTCAGATCCCCAGCTGCCTGAGAACCACCCAACCTCCTGCGAGCC	960
Db	901	TTCAAGCGGCTCATTCAGATCCCCAGCTGCCTGAGAACCACCCAACCTCCTGCGAGCC	960
Qy	961	TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCCTCATCCCC	1020
Db	961	TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCCTCATCCCC	1020
Qy	1021	GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT	1080
Db	1021	GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT	1080
Qy	1081	TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAAT	1140
Db	1081	TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAAT	1140
Qy	1141	TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC	1200
Db	1141	TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC	1200
Qy	1201	AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT	1260
Db	1201	AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT	1260
Qy	1261	GTGCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC	1320
Db	1261	GTGCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC	1320
Qy	1321	CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCCTGCGGGCAGAACTGGACGAGCTCAGG	1380
Db	1321	CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCCTGCGGGCAGAACTGGACGAGCTCAGG	1380
Qy	1381	AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT	1440
Db	1381	AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT	1440
Qy	1441	CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAAC	1500
Db	1441	CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAAC	1500
Qy	1501	CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA	1560
Db	1501	CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA	1560
Qy	1561	GCCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT	1620
Db	1561	GCCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT	1620
Qy	1621	GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA	1680
Db	1621	GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA	1680
Qy	1681	CTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCAG	1740
Db	1681	CTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCAG	1740

Qy	1741	TCAGAAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG	1800
Db	1741	TCAGAAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG	1800
Qy	1801	AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAGAAGCTGCAGGACACT	1860
Db	1801	AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAGAAGCTGCAGGACACT	1860
Qy	1861	CAGCTCAAACCTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAA	1920
Db	1861	CAGCTCAAACCTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAA	1920
Qy	1921	ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG	1980
Db	1921	ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG	1980
Qy	1981	CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC	2040
Db	1981	CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC	2040
Qy	2041	ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC	2100
Db	2041	ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC	2100
Qy	2101	CCAGAAGACATCAGTGGACTTCTCCATTCCATAAACCTGCTGGCCCCACTTGACCAGCGAC	2160
Db	2101	CCAGAAGACATCAGTGGACTTCTCCATTCCATAAACCTGCTGGCCCCACTTGACCAGCGAC	2160
Qy	2161	GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG	2220
Db	2161	GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG	2220
Qy	2221	ACCGAGGCCTGTAAGCAGTATGGCAGGGAAACCTCGCCTACCTGGCCTCCCTGGAGGAA	2280
Db	2221	ACCGAGGCCTGTAAGCAGTATGGCAGGGAAACCTCGCCTACCTGGCCTCCCTGGAGGAA	2280
Qy	2281	GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG	2340
Db	2281	GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG	2340
Qy	2341	GCCATCGGCGAGGAGCTCCTGCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGAC	2400
Db	2341	GCCATCGGCGAGGAGCTCCTGCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGAC	2400
Qy	2401	CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA	2460
Db	2401	CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA	2460
Qy	2461	GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAAT'TGGAGGTGAATGAA	2520
Db	2461	GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAAT'TGGAGGTGAATGAA	2520
Qy	2521	AGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATT'CAGGTGCTCATCGTGGCCTCT	2580
Db	2521	AGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATT'CAGGTGCTCATCGTGGCCTCT	2580

Qy	2581	AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT	2640
Db	2581	AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT	2640
Qy	2641	TATGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG	2700
Db	2641	TATGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG	2700
Qy	2701	GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG	2760
Db	2701	GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG	2760
Qy	2761	GAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCC	2820
Db	2761	GAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCC	2820
Qy	2821	AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA	2880
Db	2821	AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA	2880
Qy	2881	GTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAA	2940
Db	2881	GTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAA	2940
Qy	2941	GAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATG	3000
Db	2941	GAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATG	3000
Qy	3001	GATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAAC TG	3060
Db	3001	GATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAAC TG	3060
Qy	3061	GGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAGGA	3120
Db	3061	GGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAGGA	3120
Qy	3121	ACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACC	3180
Db	3121	ACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACC	3180
Qy	3181	AACACCCCATATGTCAGTGTAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGC	3240
Db	3181	AACACCCCATATGTCAGTGTAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGC	3240
Qy	3241	CACAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGA	3300
Db	3241	CACAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGA	3300
Qy	3301	GGACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCA	3360
Db	3301	GGACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCA	3360
Qy	3361	TGGATTTCCACTGCTTCTTATGGTGGTTGGTTGGGTTTTTTGGTTTTGTTTTTTTTTTT	3420
Db	3361	TGGATTTCCACTGCTTCTTATGGTGGTTGGTTGGGTTTTTTGGTTTTGTTTTTTTTTTT	3420
Qy	3421	AAGTTTCACTCACATAGCCAACCTCTCCCAAAGGGCACACCCCTGGGGCTGAGTCTCCAGG	3480



Db	3421	 AAGTTTCACTCACATAGCCAACCTCTCCCAAAGGGCACACCCCTGGGGCTGAGTCTCCAGG	3480
Qy	3481	 GCCCCCAACTGTGGTAGCTCCAGCGATGGTGCTGCCCAGGCCCTCTCGGTGCTCCATCTC	3540
Db	3481	 GCCCCCAACTGTGGTAGCTCCAGCGATGGTGCTGCCCAGGCCCTCTCGGTGCTCCATCTC	3540
Qy	3541	 CGCCTCCACACTGACCAAGTGCTGGCCACCCAGTCCATGCTCCAGGGTCAGGCGGAGCT	3600
Db	3541	 CGCCTCCACACTGACCAAGTGCTGGCCACCCAGTCCATGCTCCAGGGTCAGGCGGAGCT	3600
Qy	3601	 GCTGAGTGAÇAGCTTTCCTCAAAAAGCAGAAGGAGAGTGAGTGCCTTTCCCTCCTAAAGC	3660
Db	3601	 GCTGAGTGACAGCTTTCCTCAAAAAGCAGAAGGAGAGTGAGTGCCTTTCCCTCCTAAAGC	3660
Qy	3661	 TGAATCCCGGCGGAAAGCCTCTGTCCGCCTTTACAAGGGAGAAGACAACAGAAAGAGGGA	3720
Db	3661	 TGAATCCCGGCGGAAAGCCTCTGTCCGCCTTTACAAGGGAGAAGACAACAGAAAGAGGGA	3720
Qy	3721	 CAAGAGGGTTCACACAGCCCAGTTCCCGTGACGAGGCTCAAAAACCTTGATCACATGCTTG	3780
Db	3721	 CAAGAGGGTTCACACAGCCCAGTTCCCGTGACGAGGCTCAAAAACCTTGATCACATGCTTG	3780
Qy	3781	 AATGGAGCTGGTGAGATCAACAACACTACTTCCCTGCCGGAATGAAGTGTCCGTGAATGG	3840
Db	3781	 AATGGAGCTGGTGAGATCAACAACACTACTTCCCTGCCGGAATGAAGTGTCCGTGAATGG	3840
Qy	3841	 TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTGGGAGTGATTCCCAAC	3900
Db	3841	 TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTGGGAGTGATTCCCAAC	3900
Qy	3901	 TCCTTTCTGCAGACGTCTGCCTTGGCATCCTCTTGAATAGGAAGATCGTTCCACCTTCTA	3960
Db	3901	 TCCTTTCTGCAGACGTCTGCCTTGGCATCCTCTTGAATAGGAAGATCGTTCCACCTTCTA	3960
Qy	3961	 CGCAATTGACAAACCCGGAAGATCAGATGCAATTGCTCCCATCAGGGAAGAACCCTATAC	4020
Db	3961	 CGCAATTGACAAACCCGGAAGATCAGATGCAATTGCTCCCATCAGGGAAGAACCCTATAC	4020
Qy	4021	 TTGGTTTGTCTACCCTTAGTATTTATTACTAACCCTCCCTTAAGCAGCAACAGCCTACAAAG	4080
Db	4021	 TTGGTTTGTCTACCCTTAGTATTTATTACTAACCCTCCCTTAAGCAGCAACAGCCTACAAAG	4080
Qy	4081	 AGATGCTTGGAGCAATCAGAACTTCAGGTGTGACTCTAGCAAAGCTCATCTTTCTGCCCCG	4140
Db	4081	 AGATGCTTGGAGCAATCAGAACTTCAGGTGTGACTCTAGCAAAGCTCATCTTTCTGCCCCG	4140
Qy	4141	 GCTACATCAGCCTTCAAGAATCAGAAGAAAGGCCAAGGTGCTGGACTGTTACTGACTTGG	4200
Db	4141	 GCTACATCAGCCTTCAAGAATCAGAAGAAAGGCCAAGGTGCTGGACTGTTACTGACTTGG	4200
Qy	4201	 ATCCCAAAGCAAGGAGATCATTTGGAGCTCTTGGGTGAGAGAAAATGAGAAAGGACAGAG	4260
Db	4201	 ATCCCAAAGCAAGGAGATCATTTGGAGCTCTTGGGTGAGAGAAAATGAGAAAGGACAGAG	4260
Qy	4261	 CCAGCGGCTCCAACCTCCTTTTCCAGCCACATGCCCCAGGCTCTCGCTGCCCTGTGGACAGGA	4320

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Db      4261 CCAGCGGCTCCAACTCCTTTTCAGCCACATGCCCCAGGCTCTCGCTGCCCTGTGGACAGGA 4320
Qy      4321 TGAGGACAGAGGGCACATGAACAGCTTGCCAGGGATGGGCAGCCCAACAGCACTTTTCCT 4380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 TGAGGACAGAGGGCACATGAACAGCTTGCCAGGGATGGGCAGCCCAACAGCACTTTTCCT 4380
Qy      4381 CTTCTAGATGGACCCAGCATTTAAGTGACCTTCTGATCTTGGGAAAACAGCGTCTTCCT 4440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 CTTCTAGATGGACCCAGCATTTAAGTGACCTTCTGATCTTGGGAAAACAGCGTCTTCCT 4440
Qy      4441 TCTTTATCTATAGCAACTCATTGGTGGTAGCCATCAAGCACTTCGGAATTCCTGCAGCCC 4500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 TCTTTATCTATAGCAACTCATTGGTGGTAGCCATCAAGCACTTCGGAATTCCTGCAGCCC 4500
Qy      4501 GGGCGGCCGCTCGAGCATGCNNTAGAGGGCCCTA 4534
        ||||||||||||||||||||||||||||||||||||
Db      4501 GGGCGGCCGCTCGAGCATGCNNTAGAGGGCCCTA 4534

```

RESULT 2

AEB71165

ID AEB71165 standard; DNA; 4534 BP.

XX

AC AEB71165;

XX

DT 20-OCT-2005 (first entry)

XX

DE DNA encoding full length HIP1, SEQ ID NO:1.

XX

KW Cancer; cytosatic; diagnosis; genetic marker; HIP1; immunodiagnosis;  
 KW drug screening; western blot; ELISA; ds; gene.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 58. .3171

FT /\*tag= a

FT /product= "HIP1"

XX

PN WO2005072457-A2.

XX

PD 11-AUG-2005.

XX

PF 28-JAN-2005; 2005WO-US003330.

XX

PR 29-JAN-2004; 2004US-00767325.

XX

PA (UNMI ) UNIV MICHIGAN.

XX

PI Ross TS, Mizukami IF;

XX

DR WPI; 2005-582467/59.

DR P-PSDB; AEB71166.

XX

PT Detecting cancer (especially prostate or colon cancer) comprises  
 PT providing a sample from a subject suspected of having cancer, and  
 PT detecting the presence or absence of antibodies to HIP1 in the sample.

XX  
PS Disclosure; SEQ ID NO 1; 118pp; English.

XX  
CC The present invention relates to compositions and methods for cancer  
CC diagnosis, including HIP1 cancer markers. HIP1 is a cofactor in clathrin  
CC mediated trafficking. HIP1 over-expression may dysregulate growth factor  
CC receptor cell surface density or growth factor secretion, as a  
CC consequence of its role in clathrin-mediated trafficking. Specifically  
CC claimed is a method of detecting cancer by providing a sample from a  
CC subject suspected of having cancer, and detecting the presence or absence  
CC of antibodies to HIP1 in the sample. Also disclosed are methods of  
CC screening for anticancer drugs; drugs identified by the above method; and  
CC methods of treating cancer. The cancer is selected from prostate cancer  
CC and colon cancer. The detecting step comprises exposing the sample to a  
CC HIP1 antigen. It comprises a Western blot or an ELISA assay. The reagent  
CC comprises a HIP1 antigen, and a second antibody that binds to the  
CC antibodies to HIP1. The present sequence is DNA encoding full length  
CC HIP1.

XX  
SQ Sequence 4534 BP; 1176 A; 1230 C; 1232 G; 894 T; 0 U; 2 Other;

Query Match 100.0%; Score 4534; DB 14; Length 4534;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCCTGACTCGGCTCCTCGCGGCGACATG	60
Db	1	CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCCTGACTCGGCTCCTCGCGGCGACATG	60
Qy	61	GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG	120
Db	61	GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG	120
Qy	121	CGCGGGGTCTGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT	180
Db	121	CGCGGGGTCTGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT	180
Qy	181	GTCAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGA	240
Db	181	GTCAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGA	240
Qy	241	ACGTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAAC	300
Db	241	ACGTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAAC	300
Qy	301	CGCCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA	360
Db	301	CGCCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA	360
Qy	361	CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG	420
Db	361	CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG	420
Qy	421	AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC	480
Db	421	AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC	480

Qy	481	TACCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGC	540
Db	481	TACCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGC	540
Qy	541	AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTT	600
Db	541	AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTT	600
Qy	601	TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACA	660
Db	601	TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACA	660
Qy	661	GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC	720
Db	661	GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC	720
Qy	721	CTCGCCCCGCTGATCCAGGTCATCTTGACTGCAGCCACCTTTATGACTACACTGTCAAG	780
Db	721	CTCGCCCCGCTGATCCAGGTCATCTTGACTGCAGCCACCTTTATGACTACACTGTCAAG	780
Qy	781	CTTCTCTTCAAACCTCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGC	840
Db	781	CTTCTCTTCAAACCTCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGC	840
Qy	841	TTCATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC	900
Db	841	TTCATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC	900
Qy	901	TTCAAGCGGCTCATTCAGATCCCCAGCTGCCTGAGAACCCACCCAACCTCCTGCGAGCC	960
Db	901	TTCAAGCGGCTCATTCAGATCCCCAGCTGCCTGAGAACCCACCCAACCTCCTGCGAGCC	960
Qy	961	TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCC	1020
Db	961	TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCC	1020
Qy	1021	GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT	1080
Db	1021	GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT	1080
Qy	1081	TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTTCAGCAGTGATCCCTTCAAT	1140
Db	1081	TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTTCAGCAGTGATCCCTTCAAT	1140
Qy	1141	TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC	1200
Db	1141	TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC	1200
Qy	1201	AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT	1260
Db	1201	AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT	1260
Qy	1261	GTGCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC	1320
Db	1261	GTGCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC	1320
Qy	1321	CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGG	1380

Db	1321	 CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGG	1380
Qy	1381	AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT	1440
Db	1381	AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT	1440
Qy	1441	CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAAC	1500
Db	1441	CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAAC	1500
Qy	1501	CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA	1560
Db	1501	CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA	1560
Qy	1561	GCCCAGGTAGATTTGGAACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT	1620
Db	1561	GCCCAGGTAGATTTGGAACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT	1620
Qy	1621	GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA	1680
Db	1621	GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA	1680
Qy	1681	CTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAG	1740
Db	1681	CTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAG	1740
Qy	1741	TCAGAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG	1800
Db	1741	TCAGAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG	1800
Qy	1801	AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAGAAGTGCAGGACACT	1860
Db	1801	AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAGAAGTGCAGGACACT	1860
Qy	1861	CAGCTCAAACCTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAA	1920
Db	1861	CAGCTCAAACCTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAA	1920
Qy	1921	ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG	1980
Db	1921	ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG	1980
Qy	1981	CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC	2040
Db	1981	CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC	2040
Qy	2041	ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC	2100
Db	2041	ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC	2100
Qy	2101	CCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGAC	2160
Db	2101	CCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGAC	2160
Qy	2161	GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG	2220

Db	2161	GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG	2220
Qy	2221	ACCGAGGCCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCCTACCTGGCCTCCCTGGAGGAA	2280
Db	2221	ACCGAGGCCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCCTACCTGGCCTCCCTGGAGGAA	2280
Qy	2281	GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG	2340
Db	2281	GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG	2340
Qy	2341	GCCATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGAC	2400
Db	2341	GCCATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGAC	2400
Qy	2401	CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA	2460
Db	2401	CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA	2460
Qy	2461	GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAA	2520
Db	2461	GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAA	2520
Qy	2521	AGGATCCTTGTTGCTGTACCAGCCTCATGCAAGCTATTGAGGTGCTCATCGTGGCCTCT	2580
Db	2521	AGGATCCTTGTTGCTGTACCAGCCTCATGCAAGCTATTGAGGTGCTCATCGTGGCCTCT	2580
Qy	2581	AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT	2640
Db	2581	AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT	2640
Qy	2641	TATGCCAAGAAGCTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG	2700
Db	2641	TATGCCAAGAAGCTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG	2700
Qy	2701	GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG	2760
Db	2701	GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG	2760
Qy	2761	GAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCC	2820
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Qy	2821	AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA	2880
Db	2821	AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA	2880
Qy	2881	GTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAA	2940
Db	2881	GTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAA	2940
Qy	2941	GAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATG	3000
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Qy	3061	GGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAGGA	3120
Db	3061	GGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAGGA	3120
Qy	3121	ACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACC	3180
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Qy	3181	AACACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGC	3240
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Qy	3241	CACAGGCCAAATCCTTGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGA	3300
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Qy	3301	GGACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTCTGTTTGGACCCA	3360
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Qy	3361	TGGATTTCCACTGCTTCTTATGGTGGTGGTGGGTTTTTTGGTTTTGTTTTTTTTTTTT	3420
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Qy	3421	AAGTTTCACTCACATAGCCAACTCTCCCAAAGGGCACACCCCTGGGGCTGAGTCTCCAGG	3480
Db	3421	AAGTTTCACTCACATAGCCAACTCTCCCAAAGGGCACACCCCTGGGGCTGAGTCTCCAGG	3480
Qy	3481	GCCCCCAACTGTGGTAGCTCCAGCGATGGTGC'TGCCAGGCCCTCTCGGTGCTCCATCTC	3540
Db	3481	GCCCCCAACTGTGGTAGCTCCAGCGATGGTGC'TGCCAGGCCCTCTCGGTGCTCCATCTC	3540
Qy	3541	CGCCTCCACACTGACCAAGTGCTGGCCACCCAGTCCATGCTCCAGGGTCAGGCGGAGCT	3600
Db	3541	CGCCTCCACACTGACCAAGTGCTGGCCACCCAGTCCATGCTCCAGGGTCAGGCGGAGCT	3600
Qy	3601	GCTGAGTGACAGCTTTCCTCAAAAAGCAGAAGGAGAGTGAGTGCCTTTCCTCCTAAAGC	3660
Db	3601	GCTGAGTGACAGCTTTCCTCAAAAAGCAGAAGGAGAGTGAGTGCCTTTCCTCCTAAAGC	3660
Qy	3661	TGAATCCCGGCGGAAAGCCTCTGTCCGCCTTTACAAGGGAGAAGACAACAGAAAGAGGGA	3720
Db	3661	TGAATCCCGGCGGAAAGCCTCTGTCCGCCTTTACAAGGGAGAAGACAACAGAAAGAGGGA	3720
Qy	3721	CAAGAGGGTTCACACAGCCAGTTCCTCGTGACGAGGCTCAAAAACCTTGATCACATGCTTG	3780
Db	3721	CAAGAGGGTTCACACAGCCAGTTCCTCGTGACGAGGCTCAAAAACCTTGATCACATGCTTG	3780
Qy	3781	AATGGAGCTGGTGAGATCAACAACACTACTTCCCTGCCGGAATGAAGTGTCCGTGAATGG	3840
Db	3781	AATGGAGCTGGTGAGATCAACAACACTACTTCCCTGCCGGAATGAAGTGTCCGTGAATGG	3840
Qy	3841	TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTGGGAGTGATTCCCAAC	3900
Db	3841	TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTGGGAGTGATTCCCAAC	3900

Qy	3901	TCCTTTCTGCAGACGTCTGCCTTGGCATCCTCTTGAATAGGAAGATCGTTCCACCTTCTA	3960
Db	3901	TCCTTTCTGCAGACGTCTGCCTTGGCATCCTCTTGAATAGGAAGATCGTTCCACCTTCTA	3960
Qy	3961	CGCAATTGACAAACCCGGAAGATCAGATGCAATTGCTCCCATCAGGGAAGAACCCTATAC	4020
Db	3961	CGCAATTGACAAACCCGGAAGATCAGATGCAATTGCTCCCATCAGGGAAGAACCCTATAC	4020
Qy	4021	TTGGTTTGCTACCCTTAGTATTTATTACTAACCTCCCTTAAGCAGCAACAGCCTACAAAG	4080
Db	4021	TTGGTTTGCTACCCTTAGTATTTATTACTAACCTCCCTTAAGCAGCAACAGCCTACAAAG	4080
Qy	4081	AGATGCTTGGAGCAATCAGAACTTCAGGTGTGACTCTAGCAAAGCTCATCTTTCTGCCCCG	4140
Db	4081	AGATGCTTGGAGCAATCAGAACTTCAGGTGTGACTCTAGCAAAGCTCATCTTTCTGCCCCG	4140
Qy	4141	GCTACATCAGCCTTCAAGAATCAGAAGAAAGGCCAAGGTGCTGGACTGTTACTGACTTGG	4200
Db	4141	GCTACATCAGCCTTCAAGAATCAGAAGAAAGGCCAAGGTGCTGGACTGTTACTGACTTGG	4200
Qy	4201	ATCCCAAAGCAAGGAGATCATTTGGAGCTCTTGGGTCAGAGAAAATGAGAAAGGACAGAG	4260
Db	4201	ATCCCAAAGCAAGGAGATCATTTGGAGCTCTTGGGTCAGAGAAAATGAGAAAGGACAGAG	4260
Qy	4261	CCAGCGGCTCCAACCTCTTTCAGCCACATGCCCCAGGCTCTCGCTGCCCTGTGGACAGGA	4320
Db	4261	CCAGCGGCTCCAACCTCTTTCAGCCACATGCCCCAGGCTCTCGCTGCCCTGTGGACAGGA	4320
Qy	4321	TGAGGACAGAGGGCACATGAACAGCTTGCCAGGGATGGGCAGCCCAACAGCACTTTTCCT	4380
Db	4321	TGAGGACAGAGGGCACATGAACAGCTTGCCAGGGATGGGCAGCCCAACAGCACTTTTCCT	4380
Qy	4381	CTTCTAGATGGACCCAGCATTTAAGTGACCTTCTGATCTTGGGAAAACAGCGTCTTCCT	4440
Db	4381	CTTCTAGATGGACCCAGCATTTAAGTGACCTTCTGATCTTGGGAAAACAGCGTCTTCCT	4440
Qy	4441	TCTTTATCTATAGCAACTCATTGGTGGTAGCCATCAAGCACTTCGGAATTCCTGCAGCCC	4500
Db	4441	TCTTTATCTATAGCAACTCATTGGTGGTAGCCATCAAGCACTTCGGAATTCCTGCAGCCC	4500
Qy	4501	GGGCGGCCGCTCGAGCATGCNNTAGAGGGCCCTA	4534
Db	4501	GGGCGGCCGCTCGAGCATGCNNTAGAGGGCCCTA	4534

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OM nucleic - nucleic search, using sw model

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#### SUMMARIES

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1	2779	61.3	6628	3	US-09-949-016-4586	Sequence 4586, Ap		
2	2619	57.8	4796	3	US-09-085-199B-3	Sequence 3, Appli		
3	973	21.5	68702	3	US-09-949-016-16328	Sequence 16328, A		
4	955	21.1	3715	3	US-09-085-199B-44	Sequence 44, Appl		
5	907	20.0	1164	3	US-09-085-199B-1	Sequence 1, Appli		
6	187	4.1	436	3	US-09-085-199B-28	Sequence 28, Appl		
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9	148	3.3	485	3	US-09-085-199B-32	Sequence 32, Appl		
10	144	3.2	565	3	US-09-085-199B-23	Sequence 23, Appl		
11	143	3.2	578	3	US-09-085-199B-25	Sequence 25, Appl		
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14	126	2.8	418	3	US-09-085-199B-42	Sequence 42, Appl		
15	119	2.6	359	3	US-09-085-199B-30	Sequence 30, Appl		
16	114	2.5	427	3	US-09-085-199B-37	Sequence 37, Appl		
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c 19	113	2.5	601	3	US-09-949-016-163647	Sequence 163647,		
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c 21	110	2.4	601	3	US-09-949-016-163613	Sequence 163613,		

	22	108	2.4	351	3	US-09-085-199B-41	Sequence 41, Appl
	23	104	2.3	209	3	US-09-085-199B-31	Sequence 31, Appl
	24	103	2.3	437	3	US-09-085-199B-40	Sequence 40, Appl
c	25	103	2.3	601	3	US-09-949-016-163567	Sequence 163567,
	26	102	2.2	390	3	US-09-085-199B-26	Sequence 26, Appl
c	27	102	2.2	601	3	US-09-949-016-163602	Sequence 163602,
c	28	100	2.2	601	3	US-09-949-016-163634	Sequence 163634,
	29	97	2.1	502	3	US-09-085-199B-39	Sequence 39, Appl
c	30	97	2.1	601	3	US-09-949-016-163624	Sequence 163624,
c	31	97	2.1	601	3	US-09-949-016-163626	Sequence 163626,
c	32	97	2.1	601	3	US-09-949-016-163627	Sequence 163627,
	33	94	2.1	193	3	US-09-085-199B-17	Sequence 17, Appl
	34	90	2.0	393	3	US-09-085-199B-34	Sequence 34, Appl
	35	89	2.0	469	3	US-09-085-199B-29	Sequence 29, Appl
	36	77	1.7	327	3	US-09-085-199B-20	Sequence 20, Appl
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c	38	77	1.7	601	3	US-09-949-016-163584	Sequence 163584,
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	40	68	1.5	447	3	US-09-621-976-11364	Sequence 11364, A
	41	68	1.5	516	3	US-09-085-199B-16	Sequence 16, Appl
c	42	68	1.5	601	3	US-09-949-016-163562	Sequence 163562,
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c	44	67	1.5	601	3	US-09-949-016-163638	Sequence 163638,
c	45	67	1.5	601	3	US-09-949-016-163639	Sequence 163639,

#### ALIGNMENTS

##### RESULT 1

US-09-949-016-4586

; Sequence 4586, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4586

; LENGTH: 6628

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-4586

Query Match 61.3%; Score 2779; DB 3; Length 6628;  
Best Local Similarity 99.8%; Pred. No. 0;

Matches 3179; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

Qy	183	CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC	242
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Qy	243	GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG	302
Db	61	GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG	120
Qy	303	CCTGCCCTCTGTCTAGCAACGCAGTGTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT	362
Db	121	CCTGCCCTCTGTCTAGCAACGCAGTGTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT	180
Qy	363	CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG	422
Db	181	CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG	240
Qy	423	TGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA	482
Db	241	TGACATGAGCAGGATGTGGGGCCACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA	300
Qy	483	CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA	542
Db	301	CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA	360
Qy	543	CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTC	602
Db	361	CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTT	420
Qy	603	CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT	662
Db	421	CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT	480
Qy	663	ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT	722
Db	481	ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT	540
Qy	723	CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT	782
Db	541	CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT	600
Qy	783	TCTCTTCAAACCTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT	842
Db	601	TCTCTTCAAACCTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT	660
Qy	843	CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT	902
Db	661	CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT	720
Qy	903	CAAGCGGCTCATTAGATCCCCAGCTGCCTGAGAACCCACCCAACCTTCTGCGAGCCTC	962
Db	721	CAAGCGGCTCATTAGATCCCCAGCTGCCTGAGAACCCACCCAACCTTCTGCGAGCCTC	780
Qy	963	AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCGA	1022
Db	781	AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCGA	840

Qy	1023	CAGCGAGCCAGTCCCTAGAGAAGGATGACCTCATGGACATGGATGCCCTCTCAGCAGAATTT	1082
Db	841	CAGCGAGCCAGTCCCTAGAGAAGGATGACCTCATGGACATGGATGCCCTCTCAGCAGAATTT	900
Qy	1083	ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT	1142
Db	901	ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT	960
Qy	1143	CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACCTTAATTGAGCGACTATACAG	1202
Db	961	CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACCTTAATTGAGCGACTATACAG	1020
Qy	1203	AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT	1262
Db	1021	AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT	1080
Qy	1263	GCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT	1322
Db	1081	GCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT	1140
Qy	1323	GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG	1382
Db	1141	GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG	1200
Qy	1383	GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA	1442
Db	1201	GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA	1260
Qy	1443	AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA	1502
Db	1261	AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA	1320
Qy	1503	CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC	1562
Db	1321	CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC	1380
Qy	1563	CCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA	1622
Db	1381	CCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA	1440
Qy	1623	CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT	1682
Db	1441	CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT	1500
Qy	1683	TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAACTTCTGCCCAGTC	1742
Db	1501	TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAACTTCTGCCCAGTC	1560
Qy	1743	AGAAGCAAACCTGGGCAGCCGAGTTGCGCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG	1802
Db	1561	AGAAGCAAACCTGGGCAGCCGAGTTGCGCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG	1620
Qy	1803	TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA	1862
Db	1621	TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA	1680

Qy	1863	GCTCAAACCTGGCCAGCACAGAG----	GAATCTATGTGCCAGCTTGCCAAAGACCAACGAA	1918
Db	1681	GCTCAAACCTGGCCAGCACAGAGGCAAGAATCTATGTGCCAGCTTGCCAAAGACCAACGAA		1740
Qy	1919	AAATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACC		1978
Db	1741	AAATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACC		1800
Qy	1979	AGCTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGG		2038
Db	1801	AGCTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGG		1860
Qy	2039	TCACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCT		2098
Db	1861	TCACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCT		1920
Qy	2099	GCCCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCG		2158
Db	1921	GCCCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCG		1980
Qy	2159	ACGCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCAC		2218
Db	1981	ACGCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCAC		2040
Qy	2219	TGACCGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGG		2278
Db	2041	TGACCGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGG		2100
Qy	2279	AAGAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCA		2338
Db	2101	AAGAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCA		2160
Qy	2339	AGGCCATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGG		2398
Db	2161	AGGCCATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGG		2220
Qy	2399	ACCTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAA		2458
Db	2221	ACCTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAA		2280
Qy	2459	TAGAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATG		2518
Db	2281	TAGAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATG		2340
Qy	2519	AAAGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCT		2578
Db	2341	AAAGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCT		2400
Qy	2579	CTAAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGT		2638
Db	2401	CTAAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGT		2460
Qy	2639	TTTATGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCT		2698
Db	2461	TTTATGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCT		2520
Qy	2699	GGGGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTG		2758

Db	2521	 GGGGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTG	2580
Qy	2759	AGGAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCAT	2818
Db	2581	 AGGAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCAT	2640
Qy	2819	CCAAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGG	2878
Db	2641	 CCAAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGG	2700
Qy	2879	GAGTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCG	2938
Db	2701	 GAGTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCG	2760
Qy	2939	AAGAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGA	2998
Db	2761	 AAGAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGA	2820
Qy	2999	TGGATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAAC	3058
Db	2821	 TGGATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAAC	2880
Qy	3059	TGGGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAG	3118
Db	2881	 TGGGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAG	2940
Qy	3119	GAACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAA	3178
Db	2941	 GAACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAA	3000
Qy	3179	CCAACACCCCATATGTCAGTGTAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCA	3238
Db	3001	 CCAACACCCCATATGTCAGTGTAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCA	3060
Qy	3239	GCCACAGGCCAAATCCTTGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCC	3298
Db	3061	 GCCACAGGCCAAATCCTTGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCC	3120
Qy	3299	GAGGACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACC	3358
Db	3121	 GAGGACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACC	3180
Qy	3359	CATGG 3363	
Db	3181	 CATGG 3185	

GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			%		Query		ID	Description
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	1	4534	100.0	4534	6	US-10-007-047-1	Sequence 1, Appli	
	2	4534	100.0	4534	8	US-10-767-325-1	Sequence 1, Appli	
	3	3911	86.3	3911	6	US-10-007-047-3	Sequence 3, Appli	
	4	3911	86.3	3911	8	US-10-767-325-3	Sequence 3, Appli	
	5	3035	66.9	4714	9	US-10-756-149-1417	Sequence 1417, Ap	
	6	3035	66.9	6626	7	US-10-293-864-4	Sequence 4, Appli	
	7	3035	66.9	6626	9	US-10-934-998-38	Sequence 38, Appl	
	8	973	21.5	65454	7	US-10-293-864-11	Sequence 11, Appl	
	9	554	12.2	601	3	US-09-833-790-343	Sequence 343, App	
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c	11	393	8.7	393	9	US-10-934-998-139	Sequence 139, App	
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	15	163	3.6	404	6	US-10-007-047-6	Sequence 6, Appli	
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	17	143	3.2	577	3	US-09-864-761-8117	Sequence 8117, Ap	
	18	141	3.1	141	3	US-09-864-761-24860	Sequence 24860, A	
	19	141	3.1	2080	6	US-10-108-260A-387	Sequence 387, App	

c	20	126	2.8	161	6	US-10-029-386-16651	Sequence 16651, A
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	23	87	1.9	565	4	US-09-925-065A-518628	Sequence 518628,
	24	76	1.7	219	7	US-10-293-864-13	Sequence 13, Appl
	25	68	1.5	516	7	US-10-293-864-12	Sequence 12, Appl
	26	62	1.4	606	4	US-09-925-065A-600703	Sequence 600703,
	27	60	1.3	60	3	US-09-908-975-13034	Sequence 13034, A
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c	29	32	0.7	141	5	US-10-066-543-969	Sequence 969, App
c	30	31	0.7	962	3	US-09-764-886-40	Sequence 40, Appl
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	40	26	0.6	502	7	US-10-424-599-1463	Sequence 1463, Ap
	41	26	0.6	603	4	US-09-925-065A-911834	Sequence 911834,
c	42	26	0.6	656	4	US-09-925-065A-37147	Sequence 37147, A
c	43	26	0.6	732	4	US-09-925-065A-92008	Sequence 92008, A
	44	26	0.6	49888	6	US-10-085-117-25	Sequence 25, Appl
	45	25	0.6	25	7	US-10-719-956-512062	Sequence 512062,

#### ALIGNMENTS

#### RESULT 1

US-10-007-047-1

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; Sequence 1, Application US/10007047
; Publication No. US20030124533A1
; GENERAL INFORMATION:
; APPLICANT: Mizukami, Ikuko
; APPLICANT: Ross, Theodora
; APPLICANT: Rao, Dinesh
; TITLE OF INVENTION: HIP1 Cancer Markers
; FILE REFERENCE: UM-06692
; CURRENT APPLICATION NUMBER: US/10/007,047
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4534
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4521)..(4521)
; OTHER INFORMATION: The nucleotide "n" can be either a,t,c, or g
; NAME/KEY: misc_feature
; LOCATION: (4522)..(4522)
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US-10-007-047-1

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Query Match 100.0%; Score 4534; DB 6; Length 4534;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG	120
Db	61	GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG	120
Qy	121	CGCGGGGTCGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT	180
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Qy	301	CGCCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA	360
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Qy	361	CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG	420
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Qy	421	AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC	480
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Qy	541	AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTT	600
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Qy	601	TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACA	660
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Db	661	GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC	720
Qy	721	CTCGCCCCGCTGATCCAGGTCATCTTGACTGCAGCCACCTTTATGACTACACTGTCAAG	780
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Qy	841	TTCATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC	900
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Qy	901	TTCAAGCGGCTCATTAGATCCCCCAGCTGCCTGAGAACCCACCCAACCTCCTGCGAGCC	960
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Qy	961	TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCC	1020
Db	961	TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCC	1020
Qy	1021	GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT	1080
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Qy	1081	TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTAGCAGTGATCCCTTCAAT	1140
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Qy	1141	TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC	1200
Db	1141	TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC	1200
Qy	1201	AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT	1260
Db	1201	AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT	1260
Qy	1261	GTGCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC	1320
Db	1261	GTGCTGCAGCTGAAGGGCCACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC	1320
Qy	1321	CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGG	1380
Db	1321	CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGG	1380
Qy	1381	AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT	1440
Db	1381	AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT	1440
Qy	1441	CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTTCAAG	1500
Db	1441	CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTTCAAG	1500
Qy	1501	CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA	1560
Db	1501	CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA	1560
Qy	1561	GCCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT	1620
Db	1561	GCCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT	1620
Qy	1621	GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA	1680

Db	1621	 GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTC TAGAGAGCTTGAAGCAGGAA	1680
Qy	1681	CTTGCCACAAGCCAACGGGAGCTTCAGGTTCGCAAGGCAGCCTGGAAACTTCTGCCCAG	1740
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Db	1741	TCAGAAGCAAAC TGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG	1800
Qy	1801	AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAGAAGCTGCAGGACACT	1860
Db	1801	AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAGAAGCTGCAGGACACT	1860
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Db	1921	ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG	1980
Qy	1981	CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC	2040
Db	1981	CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC	2040
Qy	2041	ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC	2100
Db	2041	ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC	2100
Qy	2101	CCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGAC	2160
Db	2101	CCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGAC	2160
Qy	2161	GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG	2220
Db	2161	GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG	2220
Qy	2221	ACCGAGGCCGTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAA	2280
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Qy	2281	GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG	2340
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Db	2401	CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA	2460
Qy	2461	GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAA	2520

Db	2461	GAGGAGATGCTCAGCAAATCCCAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAA	2520
Qy	2521	AGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCT	2580
Db	2521	AGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCT	2580
Qy	2581	AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT	2640
Db	2581	AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT	2640
Qy	2641	TATGCCAAGAAGCTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG	2700
Db	2641	TATGCCAAGAAGCTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG	2700
Qy	2701	GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG	2760
Db	2701	GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG	2760
Qy	2761	GAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCC	2820
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Db	2821	AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA	2880
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Qy	2941	GAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATG	3000
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Qy	3721	CAAGAGGGTTTACACAGCCCAGTTCCTGACGAGGCTCAAAAACCTTGATCACATGCTTG	3780
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Db	3781	AATGGAGCTGGTGAGATCAACAACACTACTTCCCTGCCGGAATGAACTGTCCGTGAATGG	3840
Qy	3841	TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTTGGGAGTGATTCCCAAC	3900
Db	3841	TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTTGGGAGTGATTCCCAAC	3900
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Qy	3961	CGCAATTGACAAACCCGGAAGATCAGATGCAATTGCTCCCATCAGGGAAGAACCCTATAC	4020
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Qy      4321 TGAGGACAGAGGGCACATGAACAGCTTGCCAGGGATGGGCAGCCCAACAGCACTTTTCCT 4380
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Db      4321 TGAGGACAGAGGGCACATGAACAGCTTGCCAGGGATGGGCAGCCCAACAGCACTTTTCCT 4380

Qy      4381 CTTCTAGATGGACCCAGCATTTAAGTGACCTTCTGATCTTGGGAAAACAGCGTCTTCCT 4440
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Db      4381 CTTCTAGATGGACCCAGCATTTAAGTGACCTTCTGATCTTGGGAAAACAGCGTCTTCCT 4440

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Db      4441 TCTTTATCTATAGCAACTCATTGGTGGTAGCCATCAAGCACTTCGGAATTCCTGCAGCCC 4500

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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	3245	71.6	7239	6	US-10-955-054A-21	Sequence 21, Appl		
2	30	0.7	3391	6	US-10-750-185-64852	Sequence 64852, A		
3	30	0.7	3391	6	US-10-750-623-64852	Sequence 64852, A		
4	29	0.6	4457	6	US-10-775-169-259	Sequence 259, App		
5	25	0.6	25	7	US-11-121-849-111397	Sequence 111397,		
6	25	0.6	25	7	US-11-121-849-111398	Sequence 111398,		
7	25	0.6	25	7	US-11-121-849-111399	Sequence 111399,		
8	25	0.6	25	7	US-11-121-849-111400	Sequence 111400,		
9	25	0.6	25	7	US-11-121-849-111401	Sequence 111401,		
10	25	0.6	25	7	US-11-121-849-111402	Sequence 111402,		
11	25	0.6	25	7	US-11-121-849-111403	Sequence 111403,		
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16	24	0.5	1614	6	US-10-750-623-61247	Sequence 61247, A		
17	23	0.5	1836	6	US-10-750-185-57119	Sequence 57119, A		
18	23	0.5	1836	6	US-10-750-623-57119	Sequence 57119, A		
19	23	0.5	5152	6	US-10-240-708-74	Sequence 74, Appl		
c 20	23	0.5	187745	7	US-11-121-086-83	Sequence 83, Appl		
21	22	0.5	25	7	US-11-121-849-111396	Sequence 111396,		
22	22	0.5	201	6	US-10-995-561-63599	Sequence 63599, A		
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25	22	0.5	882	6	US-10-750-185-27597	Sequence 27597, A		
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	44	21	0.5	891	6	US-10-750-623-64853	Sequence 64853, A
	45	21	0.5	1139	6	US-10-750-185-49128	Sequence 49128, A

# ALIGNMENTS

## RESULT 1

US-10-955-054A-21

; Sequence 21, Application US/10955054A

; Publication No. US20050266420A1

; GENERAL INFORMATION:

; APPLICANT: PUSZTAI, LAJOS

; APPLICANT: SYMMANS, W. FRASER

; APPLICANT: HESS, KENNETH R.

; APPLICANT: AYERS, MARK

; APPLICANT: STEC, JAMES

; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY

; FILE REFERENCE: UTXC:880US

; CURRENT APPLICATION NUMBER: US/10/955,054A

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 7239

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-955-054A-21

Query Match 71.6%; Score 3245; DB 6; Length 7239;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3345; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	241	CCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCGCCTGCCTCTGTCTA	300
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Db	1021	 TAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTTATTTGACAACAAGT	1080
Qy	1097	TTGATGACATCTTTGGCAGTTTCATTTCAGCAGTGATCCCTTCAATTTCAACAGTCAAAATG	1156
Db	1081	 TTGATGACATCTTTGGCAGTTTCATTTCAGCAGTGATCCCTTCAATTTCAACAGTCAAAATG	1140
Qy	1157	GTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAGAGAGATCAGTGGAT	1216

Db	1141	GTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAGAGAGATCAGTGGAT	1200
Qy	1217	TGAAGGCACAGCTAGAAAAACATGAAGACTGAGAGCCAGCGGGTTGTGCTGCAGCTGAAGG	1276
Db	1201	TGAAGGCACAGCTAGAAAAACATGAAGACTGAGAGCCAGCGGGTTGTGCTGCAGCTGAAGG	1260
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Qy	1577	AACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGACCAGGGCCAGCGGA	1636
Db	1561	AACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGACCAGGGCCAGCGGA	1620
Qy	1637	AGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAAC TTGCCACAAGCCAAC	1696
Db	1621	AGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAAC TTGCCACAAGCCAAC	1680
Qy	1697	GGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTCAGAAGCAAAC TGGG	1756
Db	1681	GGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTCAGAAGCAAAC TGGG	1740
Qy	1757	CAGCCGAGTTCCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAGTGGCGCAGCTCATA	1816
Db	1741	CAGCCGAGTTCCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAGTGGCGCAGCTCATA	1800
Qy	1817	GGGAGGAGGAATTATCTGCTCTTCGGAAGAAGTGCAGGACACTCAGCTCAAAC TGGCCA	1876
Db	1801	GGGAGGAGGAATTATCTGCTCTTCGGAAGAAGTGCAGGACACTCAGCTCAAAC TGGCCA	1860
Qy	1877	GCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAATGCTTCTGGTGGGGT	1936
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Db	1921	CCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCTTGAAGAACCTCCTC	1980
Qy	1997	TCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCACATCCATTTCCAGCT	2056
Db	1981	TCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCACATCCATTTCCAGCT	2040

Qy	2057	GCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCCAGAAGACATCAGTG	2116
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Db	2101	GACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGCCATTGCTCATGGTG	2160
Qy	2177	CCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGACCGAGGCCTGTAAGC	2236
Db	2161	CCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGACCGAGGCCTGTAAGC	2220
Qy	2237	AGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGAGGGAAGCCTTGAGA	2296
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Qy	2297	ATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGCCATCGGCGAGGAGC	2356
Db	2281	ATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGCCATCGGCGAGGAGC	2340
Qy	2357	TCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCTGGTGGACAAGGAGA	2416
Db	2341	TCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCTGGTGGACAAGGAGA	2400
Qy	2417	TGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGAGGAGATGCTCAGCA	2476
Db	2401	TGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGAGGAGATGCTCAGCA	2460
Qy	2477	AATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAGGATCCTTGGTTGCT	2536
Db	2461	AATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAGGATCCTTGGTTGCT	2520
Qy	2537	GTACCAGCCTCATGCAAGCTATTGAGGTGCTCATCGTGGCCTCTAAGGACCTCCAGAGAG	2596
Db	2521	GTACCAGCCTCATGCAAGCTATTGAGGTGCTCATCGTGGCCTCTAAGGACCTCCAGAGAG	2580
Qy	2597	AGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTATGCCAAGAAGCTCTC	2656
Db	2581	AGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTATGCCAAGAAGCTCTC	2640
Qy	2657	GATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGGAGCCACTGTCATGG	2716
Db	2641	GATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGGAGCCACTGTCATGG	2700
Qy	2717	TGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGAGCTAATGGTGTGTT	2776
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Qy	3017	TGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACCTGGGAGAGCTTCGGAAAA	3076
Db	3001	TGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACCTGGGAGAGCTTCGGAAAA	3060
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Qy	3137	CTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAACACCCCATATGTCA	3196
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Qy	3197	GTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCACAGGCCAAATCCTT	3256
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Db	3241	GGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGGACATGCATGACACT	3300
Qy	3317	TCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCATGG	3363
Db	3301	TCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCATGG	3347

## RESULT 2

US-10-750-185-64852

; Sequence 64852, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DeNISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MMI1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIN version 3.1

; SEQ ID NO 64852

; LENGTH: 3391

; TYPE: DNA

; ORGANISM: Bovine 19866880385058

US-10-750-185-64852

Query Match 0.7%; Score 30; DB 6; Length 3391;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 660 AGTATTCAACTCCCTGGACATGTCCCGCTC 689  
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Db 669 AGTATTCAACTCCCTGGACATGTCCCGCTC 698

RESULT 3

US-10-750-623-64852

; Sequence 64852, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DeNISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MMI1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 64852  
; LENGTH: 3391  
; TYPE: DNA  
; ORGANISM: Bovine 19866880385058  
US-10-750-623-64852

Query Match 0.7%; Score 30; DB 6; Length 3391;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
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Qy 660 AGTATTCAACTCCCTGGACATGTCCCGCTC 689  
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RESULT 4

US-10-775-169-259

; Sequence 259, Application US/10775169  
; Publication No. US20050287532A9  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael  
; APPLICANT: Twine, Natalie  
; APPLICANT: Dorner, Andrew  
; APPLICANT: Trepicchio, William  
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo





US-11-121-849-111400  
 ; Sequence 111400, Application US/11121849  
 ; Publication No. US20050272080A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John Palma  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin  
 Embedded Samples on  
 ; TITLE OF INVENTION: Microarrays  
 ; FILE REFERENCE: 3684.1  
 ; CURRENT APPLICATION NUMBER: US/11/121,849  
 ; CURRENT FILING DATE: 2005-05-03  
 ; PRIOR APPLICATION NUMBER: 60/567,949  
 ; PRIOR FILING DATE: 2004-05-03  
 ; NUMBER OF SEQ ID NOS: 673904  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 111400  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-11-121-849-111400

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GenCore version 5.1.6  
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	4	763	16.8	939	5	BQ951181 AGENCOURT
	5	715	15.8	896	5	BU169905 AGENCOURT
	6	711	15.7	920	6	CA976174 AGENCOURT
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# ALIGNMENTS

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DEFINITION Homo sapiens HIP1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
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VERSION DQ050139.1 GI:66903338  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2730)  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees  
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)  
PUBMED 15869325  
REFERENCE 2 (bases 1 to 2730)  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.  
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/gene="HIP1"  
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ORIGIN

Query Match 38.4%; Score 1739; DB 11; Length 2730;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1739; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	992	GGAAAGCTCAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGG	1051
Qy	1493	TTCAGAACCACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGG	1552
Db	1052	TTCAGAACCACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGG	1111
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Db	1172	GCATCAGTGACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGA	1231
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Db	1292	CTGCCCAGTCAGAAGCAAACCTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACA	1351
Qy	1793	GCCTGGTGAGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAGAACTGC	1852
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Db	2132	 TGGCCTCTAAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTA	2191
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Db	2192	 AAGAGTTTTATGCCAAGAAGCTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTG	2251
Qy	2693	TGGGCTGGGGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGA	2752
Db	2252	 TGGGCTGGGGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGA	2311
Qy	2753	AATTTGAGGAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGG	2812
Db	2312	 AATTTGAGGAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGG	2371
Qy	2813	CTGCATCCAAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCT	2872
Db	2372	 CTGCATCCAAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCT	2431
Qy	2873	CTCGGGGAGTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCAC	2932
Db	2432	 CTCGGGGAGTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCAC	2491
Qy	2933	AGATCGAAGAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCC	2992
Db	2492	 AGATCGAAGAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCC	2551
Qy	2993	AAGAGATGGATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTC	3052
Db	2552	 AAGAGATGGATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTC	2611
Qy	3053	AAAAACTGGGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGG	3112

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Db      2612 AAAAAGGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGG 2671
Qy      3113 AAGAAGGAACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAG 3171
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Db      2672 AAGAAGGAACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAG 2730

```

## RESULT 2

CD251809

LOCUS CD251809 867 bp mRNA linear EST 22-MAY-2003

DEFINITION AGENCOURT\_14205955 NIH\_MGC\_180 Homo sapiens cDNA clone  
IMAGE:30383286 5', mRNA sequence.

ACCESSION CD251809

VERSION CD251809.1 GI:31012275

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 867)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

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Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM446 row: o column: 07

High quality sequence start: 3

High quality sequence stop: 695.

FEATURES

source

Location/Qualifiers

1..867

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30383286"

/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"

/clone\_lib="NIH\_MGC\_180"

/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site\_1: NotI;

Site\_2: EcoRV (destroyed); Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.68 kb. Library was

constructed by (Invitrogen). Note: this is a NIH\_MGC

Library."

ORIGIN

Query Match 17.8%; Score 809; DB 6; Length 867;

Best Local Similarity 100.0%; Pred. No. 0;

	Matches	809;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1115	GTTCATT	CAGCAGT	GATCCCTT	CAATTT	CAACAGT	CAAAAT	GGTGT	GAACA	AAGGATGAGA 1174
Db	29	GTTCATT	CAGCAGT	GATCCCTT	CAATTT	CAACAGT	CAAAAT	GGTGT	GAACA	AAGGATGAGA 88
Qy	1175	AGGACCA	CTTAATT	GAGCGAC	TATACAG	AGAGAT	CAGTGGAT	TGAAGG	CACAGCT	AGAAA 1234
Db	89	AGGACCA	CTTAATT	GAGCGAC	TATACAG	AGAGAT	CAGTGGAT	TGAAGG	CACAGCT	AGAAA 148
Qy	1235	ACATGA	AAGACT	GAGAGCC	AGCGGGT	TGTGCT	GCAGCT	GAAGGG	CCACGT	CAGCGAGCTGG 1294
Db	149	ACATGA	AAGACT	GAGAGCC	AGCGGGT	TGTGCT	GCAGCT	GAAGGG	CCACGT	CAGCGAGCTGG 208
Qy	1295	AAGCAG	ATCTGG	CCGAGC	AGCAGCA	CTGCGG	CAGCAGG	CGGCCG	ACGACT	GTGAATTCC 1354
Db	209	AAGCAG	ATCTGG	CCGAGC	AGCAGCA	CTGCGG	CAGCAGG	CGGCCG	ACGACT	GTGAATTCC 268
Qy	1355	TGCGGG	CAGAACT	GGACGAG	CTCAGG	AGGCAG	CGGGAGG	ACACCG	GAGAAGG	CTCAGCGGA 1414
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Qy	1415	GCCTGT	CTGAGAT	AGAAAGG	AAAGCT	CAAGCCA	ATGAAC	AGCGAT	ATAGCA	AAGCTAAAGG 1474
Db	329	GCCTGT	CTGAGAT	AGAAAGG	AAAGCT	CAAGCCA	ATGAAC	AGCGAT	ATAGCA	AAGCTAAAGG 388
Qy	1475	AGAAGT	ACAGCG	AGCTGGT	TCAGA	ACCACG	CTGACCT	GCTGCG	GAAGA	ATGCAGAGGTGA 1534
Db	389	AGAAGT	ACAGCG	AGCTGGT	TCAGA	ACCACG	CTGACCT	GCTGCG	GAAGA	ATGCAGAGGTGA 448
Qy	1535	CCAAAC	AGGTGT	CCATGG	CCAGACA	AGCCC	AGGTAG	ATTTG	GAAAC	GAGAGAAAAAAGAGC 1594
Db	449	CCAAAC	AGGTGT	CCATGG	CCAGACA	AGCCC	AGGTAG	ATTTG	GAAAC	GAGAGAAAAAAGAGC 508
Qy	1595	TGGAGG	ATTTCG	TGGAG	CGCAT	CAGTGAC	CAGGGCC	CAGCGG	AAGACT	CAAGAACAGCTGG 1654
Db	509	TGGAGG	ATTTCG	TGGAG	CGCAT	CAGTGAC	CAGGGCC	CAGCGG	AAGACT	CAAGAACAGCTGG 568
Qy	1655	AAGTTCT	AGAGAG	CTTGA	AGCAGG	AACTTG	CCACA	AGCCA	ACGGG	AGCTTCAGGTTCTGC 1714
Db	569	AAGTTCT	AGAGAG	CTTGA	AGCAGG	AACTTG	CCACA	AGCCA	ACGGG	AGCTTCAGGTTCTGC 628
Qy	1715	AAGGCAG	CC	TGGAACT	TCTGCC	CAGTCAG	AAGCAA	ACTGGG	CAGCCG	AGTTCGCCGAGC 1774
Db	629	AAGGCAG	CC	TGGAACT	TCTGCC	CAGTCAG	AAGCAA	ACTGGG	CAGCCG	AGTTCGCCGAGC 688
Qy	1775	TAGAGA	AAGGAG	CGGGAC	AGCCTGG	TGAGTGG	CGCAGCT	CATAGG	GAGGAG	GAATTATCTG 1834
Db	689	TAGAGA	AAGGAG	CGGGAC	AGCCTGG	TGAGTGG	CGCAGCT	CATAGG	GAGGAG	GAATTATCTG 748
Qy	1835	CTCTTC	CGGAA	GAAGT	GCAGG	AACTCAG	CTCAA	ACTGGC	CAGCAC	AGAGGAATCTATGT 1894
Db	749	CTCTTC	CGGAA	GAAGT	GCAGG	AACTCAG	CTCAA	ACTGGC	CAGCAC	AGAGGAATCTATGT 808
Qy	1895	GCCAGCT	TGCCAA	AGACCA	ACGAAAA	TG 1923				
Db	809	GCCAGCT	TGCCAA	AGACCA	ACGAAAA	TG 837				